

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Waldman, Scott A.
Pearlman, Joshua M.
Barber, Michael T.
Schultz, Stephanie
Parkinson, Scott J.
- (ii) TITLE OF INVENTION: COMPOSITIONS THAT SPECIFICALLY BIND TO
COLORECTAL CANCER CELLS AND METHODS OF
USING THE SAME
- (iii) NUMBER OF SEQUENCES: 82
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris LLP
(B) STREET: One Liberty Place - 46th Floor
(C) CITY: Philadelphia
(D) STATE: PA
(E) COUNTRY: U.S.A.
(F) ZIP: 19103
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch disk, 1.44 Mb
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPerfect 6.1
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: Not Yet Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION: N/A
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1636 bases
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | |
|---|-----|
| GGGCACAAGG AGTATGGTTC TAACGTGATT GGGGTCATGA AGACGTTGCT GTTGGACTTG | 60 |
| GCTTTGTGGT CACTGCTCTT CCATCCCGGG TGGCTGTCCT TTAGTTCCCA GGCCTAAATG | 120 |
| TGACTGTGAA CGCTACTTTC ATGTATTCGG ATGGTCTGAT TCATAACTCA GCGGACTGCC | 180 |
| GGAGTAGCAC CTGTGAAGGC CTCGACCTAC TCAGGAAAT TTCAAATGCA CAACGGATGG | 240 |
| GCTGTGTCCT CATAGGGCCC TCATGTACAT ACTCCACCTT CCAGATGTAC CTTGACACAG | 300 |
| AATTGAGCTA CCCCATGATC TCAGCTGGAA GTTTTGGATT GTCATGTGAC TATAAAGAAA | 360 |

CCTTAACCAG GCTGATGTCT CCAGCTAGAA AGTTGATATA CTTCTTGGTT AACTTTTGGGA	420
AAACCAACGA TCTGCCCTTC AAAACTTATT CCTGGAGCAC TTCGTATGTT TACAAGAATG	480
GTACAGAAAC TGAGGGACTG TTTCTGGTAC CTTAATGCTC TGGAGGCTAG CGTTTCCTAT	540
TTCTCCCACG AACTCGGCTT TAAGGTGGTG TTAAGACAAG ATAAGGAGTT TCAGGATATC	600
TTAATGGACC ACAACAGGAA AAGCAATGTG ATTATTATGT GTGGTGGTCC AGAGTTCCTC	660
TACAAGCTGA AGGGTGACCG AGCAGTGGCT GAAGACATTG TCATTATTCT AGTGGATCTT	720
TTCAATGACC AGTACTTGA GGACAATGTC ACAGCCCCTG ACTATATGAA AAATGTCCTT	780
GTTCTGACGC TGTCTCCTGG GGAATTCCCT TCTAAATAGC TCTTTCTCCA GGAATCTATC	840
ACCAACAAAA CGAGACTTTG CTCTTGCCCTA TTTGAATGGA ATCCTGCTCT TTGGACATAT	900
GCTGAAGATA TTTCTTGAAA ATGGAGAAAA TATTACCACC CCCAAATTTG CTCATGCTTT	960
CAGGAATCTC ACTTTTGAAG GGTATGACGG TCCAGTGACC TTGGGATGAC TGGGGGGATG	1020
TTGACAGTAC CATGGTGCTT CCGTTATACC CTCTGTGGAC ACCAAGAAAT ACAAGGTTCT	1080
TTGGACCTAT GATACCCACG TTAATAAGAA CTATCCTGTG GATATGAGCC CCACATTAC	1140
TTGAAGAAC TCTAAACTTC CTAATGATAT TACAGGCCCG GGCCCTCAGA TCCTGATGAT	1200
TGCAGTCTTC ACCCTCACTG GAGCTGTGGT GCTGCTCCTG CTCGTCGCTC TCCTGATGCT	1260
CAGAAAATAT AGAAAAGATT ATGAACTTCG TCAGAAAAAA TGGTCCCACA TTCCTCCTGA	1320
AAATATCTTT CCTCTGGAGA CCAATGAGAC CAATCATGTT AGCCTCAAGA TCGATGATGA	1380
CAAAAGACGA GATACAATCC AGAGACTACG ACAGTGCAAA TACGACAAAA AGCGAGTGAT	1440
TCTCAAAGAT CTCAAGCACA ATGATGGTAA TTTCCTGAA AACAGAAGA TAGAATTGAA	1500
CAAGTTGCTT CAGAAAGACT ATTACAACCT GACCAAGTTC TACGGCACAG TGAAACTTGA	1560
TACCATGATC TTCGGGGTGA TAGAATACTG TGAGAGAGGA TCCCCTCCGG GAAGTTTAA	1620
ATGACACAAT TTCCTA	1636

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATG AAG ACG TTG CTG TTG GAC TTG GCT TTG TGG TCA CTG CTC TTC	45
Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe	
1 5 10 15	
CAT CCC GGG TGG CTG TCC TTT AGT TCC CAG GCC	78
His Pro Gly Trp Leu Ser Phe Ser Ser Gln Ala	
20 25	

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Thr Leu Leu Leu Asp Leu Ala Leu Trp Ser Leu Leu Phe
 1 5 10 15
 His Pro Gly Trp Leu Ser Phe Ser Ser Gln Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG TAT TCG GAT GGT CTG ATT CAT AAC TCA GGC GAC TGC CGG AGT	45
Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg Ser	
1 5 10 15	
AGC ACC TGT GAA GGC CTC GAC CTA CTC AGG AAA ATT TCA AAT GCA	90
Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala	
20 25 30	
CAA CGG ATG GGC TGT GTC CTC ATA GGG CCC TCA TGT ACA TAC TCC	135
Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser	
35 40 45	
ACC TTC CAG ATG TAC CTT GAC ACA GAA TTG AGC TAC CCC ATG ATC	180
Thr Phe Gln Met Tyr Leu Asp Thr Glu Leu Ser Tyr Pro Met Ile	
50 55 60	
TCA GCT GGA AGT TTT GGA TTG TCA TGT GAC TAT AAA GAA ACC TTA	225
Ser Ala Gly Ser Phe Gly Leu Ser Cys Asp Tyr Lys Glu Thr Leu	
65 70 75	
ACC AGG CTG ATG TCT CCA GCT AGA AAG TTG ATA TAC TTC TTG GTT	270
Thr Arg Leu Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val	
80 85 90	
AAC TTT TGG AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT TCC TGG	315
Asn Phe Trp Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp	
95 100 105	
AGC ACT TCG TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG GGA CTG	360
Ser Thr Ser Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu	
110 115 120	
TTT CTG GTA CCT	372
Phe Leu Val Pro	

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 124 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Tyr Ser Asp Gly Leu Ile His Asn Ser Gly Asp Cys Arg Ser
 1 5 10 15
 Ser Thr Cys Glu Gly Leu Asp Leu Leu Arg Lys Ile Ser Asn Ala
 20 25 30
 Gln Arg Met Gly Cys Val Leu Ile Gly Pro Ser Cys Thr Tyr Ser
 35 40 45

[illegible]

(2) INFORMATION FOR SEO ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

[illegible]

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Cys	Val	Leu	Ile	Gly	Pro	Ser	Cys	Thr	Tyr	Ser	Thr	Phe
1				5					10					15
Gln	Met	Tyr	Leu	Asp	Thr	Glu	Leu	Ser	Tyr	Pro	Met	Ile	Ser	Ala
				20					25					30

[illegible]

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

[illegible]

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Tyr	Leu	Asp	Thr	Glu	Leu	Ser	Tyr	Pro	Met	Ile	Ser	Ala	Gly
1				5					10					15
Ser	Phe	Gly	Leu	Ser	Cys	Asp	Tyr	Lys	Glu	Thr	Leu	Thr	Arg	Leu
				20					25					30
Met	Ser	Pro	Ala	Arg	Lys	Leu	Ile	Tyr	Phe	Leu	Val	Asn	Phe	Trp
				35					40					45
Lys	Thr	Asn	Asp	Leu	Pro	Phe	Lys	Thr	Tyr	Ser	Trp	Ser	Thr	Ser
				50					55					60
Tyr	Val	Tyr	Lys	Asn	Gly	Thr	Glu	Thr	Glu	Gly	Leu	Phe	Leu	Val

65 70 75
Pro

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG	ATC	TCA	GCT	GGA	AGT	TTT	GGA	TTG	TCA	TGT	GAC	TAT	AAA	GAA	45
Met	Ile	Ser	Ala	Gly	Ser	Phe	Gly	Leu	Ser	Cys	Asp	Tyr	Lys	Glu	
1				5				10						15	
ACC	TTA	ACC	AGG	CTG	ATG	TCT	CCA	GCT	AGA	AAG	TTG	ATA	TAC	TTC	90
Thr	Leu	Thr	Arg	Leu	Met	Ser	Pro	Ala	Arg	Lys	Leu	Ile	Tyr	Phe	
				20				25						30	
TTG	GTT	AAC	TTT	TGG	AAA	ACC	AAC	GAT	CTG	CCC	TTC	AAA	ACT	TAT	135
Leu	Val	Asn	Phe	Trp	Lys	Thr	Asn	Asp	Leu	Pro	Phe	Lys	Thr	Tyr	
				35				40						45	
TCC	TGG	AGC	ACT	TCG	TAT	GTT	TAC	AAG	AAT	GGT	ACA	GAA	ACT	GAG	180
Ser	Trp	Ser	Thr	Ser	Tyr	Val	Tyr	Lys	Asn	Gly	Thr	Glu	Thr	Glu	
				50				55						60	
GGA	CTG	TTT	CTG	GTA	CCT										198
Gly	Leu	Phe	Leu	Val	Pro										
				65											

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Ile	Ser	Ala	Gly	Ser	Phe	Gly	Leu	Ser	Cys	Asp	Tyr	Lys	Glu	
1				5				10						15	
Thr	Leu	Thr	Arg	Leu	Met	Ser	Pro	Ala	Arg	Lys	Leu	Ile	Tyr	Phe	
				20				25						30	
Leu	Val	Asn	Phe	Trp	Lys	Thr	Asn	Asp	Leu	Pro	Phe	Lys	Thr	Tyr	
				35				40						45	
Ser	Trp	Ser	Thr	Ser	Tyr	Val	Tyr	Lys	Asn	Gly	Thr	Glu	Thr	Glu	
				50				55						60	
Gly	Leu	Phe	Leu	Val	Pro										
				65											

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG	TCT	CCA	GCT	AGA	AAG	TTG	ATA	TAC	TTC	TTG	GTT	AAC	TTT	TGG	45
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	----

Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp
 1 5 10 15
 AAA ACC AAC GAT CTG CCC TTC AAA ACT TAT TCC TGG AGC ACT TCG 90
 Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser
 20 25 30
 TAT GTT TAC AAG AAT GGT ACA GAA ACT GAG GGA CTG TTT CTG GTA 135
 Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val
 35 40 45
 CCT 138
 Pro

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 46 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Ser Pro Ala Arg Lys Leu Ile Tyr Phe Leu Val Asn Phe Trp
 1 5 10 15
 Lys Thr Asn Asp Leu Pro Phe Lys Thr Tyr Ser Trp Ser Thr Ser
 20 25 30
 Tyr Val Tyr Lys Asn Gly Thr Glu Thr Glu Gly Leu Phe Leu Val
 35 40 45
 Pro

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ATG CAC AAC GGA TGG GCT GTG TCC TCA 27
 Met His Asn Gly Trp Ala Val Ser Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met His Asn Gly Trp Ala Val Ser Ser
 1 5

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATG TAC ATA CTC CAC CTT CCA GAT GTA CCT 30

Met Tyr Ile Leu His Leu Pro Asp Val Pro
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:17:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Tyr Ile Leu His Leu Pro Asp Val Pro
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:18:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATG TTT ACA AGA ATG GTA CAG AAA CTG AGG GAC TGT TTC TGG TAC	45
Met Phe Thr Arg Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr	15
1 5 10	
CTT AAT GCT CTG GAG GCT AGC GTT TCC TAT TTC TCC CAC GAA CTC	90
Leu Asn Ala Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu	30
20 25	
GGC TTT AAG GTG GTG TTA AGA CAA GAT AAG GAG TTT CAG GAT ATC	135
Gly Phe Lys Val Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile	45
35 40	
TTA ATG GAC CAC AAC AGG AAA AGC AAT GTG ATT ATT ATG TGT GGT	180
Leu Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly	60
50 55	
GGT CCA GAG TTC CTC TAC AAG CTG AAG GGT GAC CGA GCA GTG GCT	225
Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala	75
65 70	
GAA GAC ATT GTC ATT ATT CTA GTG GAT CTT TTC AAT GAC CAG TAC	270
Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr	90
80 85	
TTG GAG GAC AAT GTC ACA GCC CCT GAC TAT ATG AAA AAT GTC CTT	315
Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu	105
95 100	
GTT CTG ACG CTG TCT CCT GGG GAA TTC CCT TCT AAA	351
Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys	115
110	

- (2) INFORMATION FOR SEQ ID NO:19:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 117 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Met Phe Thr Arg Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr
 1 5 10 15

Leu Asn Ala Leu Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu
 20 25 30

Gly	Phe	Lys	Val	Val 35	Leu	Arg	Gln	Asp	Lys 40	Glu	Phe	Gln	Asp	Ile 45
Leu	Met	Asp	His	Asn 50	Arg	Lys	Ser	Asn	Val 55	Ile	Ile	Met	Cys	Gly 60
Gly	Pro	Glu	Phe	Leu 65	Tyr	Lys	Leu	Lys	Gly 70	Asp	Arg	Ala	Val	Ala 75
Glu	Asp	Ile	Val	Ile 80	Ile	Leu	Val	Asp	Leu 85	Phe	Asn	Asp	Gln	Tyr 90
Leu	Glu	Asp	Asn	Val 95	Thr	Ala	Pro	Asp	Tyr 100	Met	Lys	Asn	Val	Leu 105
Val	Leu	Thr	Leu	Ser 110	Pro	Gly	Glu	Phe	Pro 115	Ser	Lys			

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:20:

[illegible]

(2) INFORMATION FOR SEQ ID NO:21:

(2) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Met Val Gln Lys Leu Arg Asp Cys Phe Trp Tyr Leu Asn Ala Leu
 1 5 10 15
 Glu Ala Ser Val Ser Tyr Phe Ser His Glu Leu Gly Phe Lys Val
 20 25 30
 Val Leu Arg Gln Asp Lys Glu Phe Gln Asp Ile Leu Met Asp His
 35 40 45
 Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly Pro Glu Phe
 50 55 60
 Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu Asp Ile Val
 65 70 75
 Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu Glu Asp Asn
 80 85 90
 Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val Leu Thr Leu
 95 100 105
 Ser Pro Gly Glu Phe Pro Ser Lys
 110

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ATG GAC CAC AAC AGG AAA AGC AAT GTG ATT ATT ATG TGT GGT GGT 45
 Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly
 1 5 10 15
 CCA GAG TTC CTC TAC AAG CTG AAG GGT GAC CGA GCA GTG GCT GAA 90
 Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu
 20 25 30
 GAC ATT GTC ATT ATT CTA GTG GAT CTT TTC AAT GAC CAG TAC TTG 135
 Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu
 35 40 45
 GAG GAC AAT GTC ACA GCC CCT GAC TAT ATG AAA AAT GTC CTT GTT 180
 Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val
 50 55 60
 CTG ACG CTG TCT CCT GGG GAA TTC CCT TCT AAA 213
 Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
 65 70

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Met Asp His Asn Arg Lys Ser Asn Val Ile Ile Met Cys Gly Gly
 1 5 10 15
 Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg Ala Val Ala Glu
 20 25 30

Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn Asp Gln Tyr Leu
35 40 45

Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys Asn Val Leu Val
50 55 60

Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
65 70

(2) INFORMATION FOR SEO ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 180 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATG TGT GGT GGT CCA GAG TTC CTC TAC AAG CTG AAG GGT GAC CGA 45
Met Cys Gly Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg
1 5 10 15

GCA GTG GCT GAA GAC ATT GTC ATT ATT CTA GTG GAT CTT TTC AAT 90
Ala Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn
20 25 30

GAC CAG TAC TTG GAG GAC AAT GTC ACA GCC CCT GAC TAT ATG AAA 135
Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys
35 40 45

AAT GTC CTT GTT CTG ACG CTG TCT CCT GGG GAA TTC CCT TCT AAA 180
Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Cys Gly Gly Pro Glu Phe Leu Tyr Lys Leu Lys Gly Asp Arg
1 5 10 15

Ala Val Ala Glu Asp Ile Val Ile Ile Leu Val Asp Leu Phe Asn
20 25 30

Asp Gln Tyr Leu Glu Asp Asn Val Thr Ala Pro Asp Tyr Met Lys
35 40 45

Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro Ser Lys
50 55 60

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ATG AAA AAT GTC CTT GTT CTG ACG CTG TCT CCT GGG GAA TTC CCT 45
Met Lys Asn Val Leu Val Leu Thr Leu Ser Pro Gly Glu Phe Pro
1 5 10 15

TCT AAA 51
Ser Lys

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 17 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met	Lys	Asn	Val	Leu	Val	Leu	Thr	Leu	Ser	Pro	Gly	Glu	Phe	Pro
1				5					10					15

Ser Lys

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG	CTC	TGG	AGG	CTA	GCG	TTT	CCT	ATT	TCT	CCC	ACG	AAC	TCG	GCT	45
Met	Leu	Trp	Arg	Leu	Ala	Phe	Pro	Ile	Ser	Pro	Thr	Asn	Ser	Ala	
1				5					10					15	

TTA	AGG	TGG	TGT												57
Leu	Arg	Trp	Cys												

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met	Leu	Trp	Arg	Leu	Ala	Phe	Pro	Ile	Ser	Pro	Thr	Asn	Ser	Ala
1				5					10					15

Leu Arg Trp Cys

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATG	ACC	AGT	ACT	TGG	AGG	ACA	ATG	TCA	CAG	CCC	CTG	ACT	ATA	42
Met	Thr	Ser	Thr	Trp	Arg	Thr	Met	Ser	Gln	Pro	Leu	Thr	Ile	
1				5					10					

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Met	Thr	Ser	Thr	Trp	Arg	Thr	Met	Ser	Gln	Pro	Leu	Thr	Ile
1				5					10				

- (2) INFORMATION FOR SEQ ID NO:32:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ATG TCA CAG CCC CTG ACT ATA 21
 Met Ser Gln Pro Leu Thr Ile
 1 5

- (2) INFORMATION FOR SEQ ID NO:33:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Met Ser Gln Pro Leu Thr Ile
 1 5

- (2) INFORMATION FOR SEQ ID NO:34:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

ATG GAA TCC TGC TCT TTG GAC ATA TGC 27
 Met Glu Ser Cys Ser Leu Asp Ile Cys
 1 5

- (2) INFORMATION FOR SEQ ID NO:35:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Met Glu Ser Cys Ser Leu Asp Ile Cys
 1 5

- (2) INFORMATION FOR SEQ ID NO:36:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ATG CTG AAG ATA TTT CTT GAA AAT GGA GAA AAT ATT ACC ACC CCC 45
 Met Leu Lys Ile Phe Leu Glu Asn Gly Glu Asn Ile Thr Thr Pro
 1 5 10 15

AAA TTT GCT CAT GCT TTC AGG AAT CTC ACT TTT GAA GGG TAT GAC 90
 Lys Phe Ala His Phe Arg Asn Leu Thr Phe Glu Gly Tyr Asp
 20 25 30

GGT CCA GTG ACC TTG GGA 108
 Gly Pro Val Thr Leu Gly
 35

- (2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

ATG	CTG	AAG	ATA	TTT	CTT	GAA	AAT	GGA	GAA	AAT	ATT	ACC	ACC	CCC	45
Met	Leu	Lys	Ile	Phe	Leu	Glu	Asn	Gly	Glu	Asn	Ile	Thr	Thr	Pro	
1				5					10					15	
AAA	TTT	GCT	CAT	GCT	TTC	AGG	AAT	CTC	ACT	TTT	GAA	GGG	TAT	GAC	90
Lys	Phe	Ala	His	Ala	Phe	Arg	Asn	Leu	Thr	Phe	Glu	Gly	Tyr	Asp	
				20					25					30	
GGT	CCA	GTG	ACC	TTG	GGA										108
Gly	Pro	Val	Thr	Leu	Gly										
				35											

- (2) INFORMATION FOR SEQ ID NO:38:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 75 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

ATG	GAG	AAA	ATA	TTA	CCA	CCC	CCA	AAT	TTG	CTC	ATG	CTT	TCA	GGA	45
Met	Glu	Lys	Ile	Leu	Pro	Pro	Pro	Asn	Leu	Leu	Met	Leu	Ser	Gly	
1				5					10					15	
ATC	TCA	CTT	TTG	AAG	GGT	ATG	ACG	GTC	CAG						75
Ile	Ser	Leu	Leu	Lys	Gly	Met	Thr	Val	Gln						
				20					25						

- (2) INFORMATION FOR SEQ ID NO:39:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Met	Glu	Lys	Ile	Leu	Pro	Pro	Pro	Asn	Leu	Leu	Met	Leu	Ser	Gly	
1				5					10					15	
Ile	Ser	Leu	Leu	Lys	Gly	Met	Thr	Val	Gln						
				20					25						

- (2) INFORMATION FOR SEQ ID NO:40:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATG	CTT	TCA	GGA	ATC	TCA	CTT	TTG	AAG	GGT	ATG	ACG	GTC	CAG	42
Met	Leu	Ser	Gly	Ile	Ser	Leu	Leu	Lys	Gly	Met	Thr	Val	Gln	
1				5					10					

- (2) INFORMATION FOR SEQ ID NO:41:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Met Leu Ser Gly Ile Ser Leu Leu Lys Gly Met Thr Val Gln
 1 5 10

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ATG ACT GGG GGG ATG TTG ACA GTA CCA TGG TGC TTC CGT TAT ACC 45
 Met Thr Gly Gly Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr
 1 5 10 15

CTC TGT GGA CAC CAA GAA ATA CAA GGT TCT TTG GAC CTA 84
 Leu Cys Gly His Gln Glu Ile Gln Gly Ser Leu Asp Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Met Thr Gly Gly Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr
 1 5 10 15

Leu Cys Gly His Gln Glu Ile Gln Gly Ser Leu Asp Leu
 20 25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATG TTG ACA GTA CCA TGG TGC TTC CGT TAT ACC CTC TGT GGA CAC 45
 Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr Leu Cys Gly His
 1 5 10 15

CAA GAA ATA CAA GGT TCT TTG GAC CTA 72
 Gln Glu Ile Gln Gly Ser Leu Asp Leu
 20

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Leu Thr Val Pro Trp Cys Phe Arg Tyr Thr Leu Cys Gly His
 1 5 10 15

Gln Glu Ile Gln Gly Ser Leu Asp Leu
 20

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ATG	GTG	CTT	CCG	TTA	TAC	CCT	CTG	TGG	ACA	CCA	AGA	AAT	ACA	AGG	45
Met	Val	Leu	Pro	Leu	Tyr	Pro	Leu	Trp	Thr	Pro	Arg	Asn	Thr	Arg	
1				5				10						15	
TTC	TTT	GGA	CCT	ATG	ATA	CCC	ACG	TTA	ATA	AGA	ACT	ATC	CTG	TGG	90
Phe	Phe	Gly	Pro	Met	Ile	Pro	Thr	Leu	Ile	Arg	Thr	Ile	Leu	Trp	
				20				25						30	
ATA															93
Ile															

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Met	Val	Leu	Pro	Leu	Tyr	Pro	Leu	Trp	Thr	Pro	Arg	Asn	Thr	Arg		
1				5				10						15		
Phe	Phe	Gly	Pro	Met	Ile	Pro	Thr	Leu	Ile	Arg	Thr	Ile	Leu	Trp		
				20				25						30		
Ile																

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

ATG	ATA	CCC	ACG	TTA	ATA	AGA	ACT	ATC	CTG	TGG	ATA	36
Met	Ile	Pro	Thr	Leu	Ile	Arg	Thr	Ile	Leu	Trp	Ile	
1				5				10				

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Met	Ile	Pro	Thr	Leu	Ile	Arg	Thr	Ile	Leu	Trp	Ile	
1				5				10				

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ATG	AGC	CCC	ACA	TTC	ACT	TGG	AAG	AAC	TCT	AAA	CTT	CCT	AAT	GAT	45
Met	Ser	Pro	Thr	Phe	Thr	Trp	Lys	Asn	Ser	Lys	Leu	Pro	Asn	Asp	

1	5	10	15	
ATT ACA GGC CGG GGC CCT CAG ATC CTG ATG ATT GCA GTC TTC ACC				90
Ile Thr Gly Arg Gly Pro Gln Ile Leu Met Ile Ala Val Phe Thr	20	25	30	
CTC ACT GGA GCT GTG GTG CTG CTC CTG CTC GTC GCT CTC CTG ATG				135
Leu Thr Gly Ala Val Val Leu Leu Leu Leu Val Ala Leu Leu Met	35	40	45	
CTC AGA AAA TAT AGA AAA GAT TAT GAA CTT CGT CAG AAA AAA TGG				180
Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp	50	55	60	
TCC CAC ATT CCT CCT GAA AAT ATC TTT CCT CTG GAG ACC AAT GAG				225
Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu	65	70	75	
ACC AAT CAT GTT AGC CTC AAG ATC GAT GAT GAC AAA AGA CGA GAT				270
Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp	80	85	90	
ACA ATC CAG AGA CTA CGA CAG TGC AAA TAC GAC AAA AAG CGA GTG				315
Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val	95	100	105	
ATT CTC AAA GAT CTC AAG CAC AAT GAT GGT AAT TTC ACT GAA AAA				360
Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys	110	115	120	
CAG AAG ATA GAA TTG AAC AAG TTG CTT CAG AAA GAC TAT TAC AAC				405
Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn	125	130	135	
CTG ACC AAG TTC TAC GGC ACA GTG AAA CTT GAT ACC ATG ATC TTC				450
Leu Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe	140	145	150	
GGG GTG ATA GAA TAC TGT GAG AGA GGA TCC CCT CCG GGA AGT TTT				495
Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser Phe	155	160	165	
AAA				498
Lys				

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Met Ser Pro Thr Phe Thr Trp Lys Asn Ser Lys Leu Pro Asn Asp				
1	5	10	15	
Ile Thr Gly Arg Gly Pro Gln Ile Leu Met Ile Ala Val Phe Thr				
	20	25	30	
Leu Thr Gly Ala Val Val Leu Leu Leu Leu Val Ala Leu Leu Met				
	35	40	45	
Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys Trp				
	50	55	60	
Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn Glu				

	65		70		75
Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg Asp	80		85		90
Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg Val	95		100		105
Ile Leu Lys Asp Leu Lys His Asn Asp Gly Asn Phe Thr Glu Lys	110		115		120
Gln Lys Ile Glu Leu Asn Lys Leu Leu Gln Lys Asp Tyr Tyr Asn	125		130		135
Leu Thr Lys Phe Tyr Gly Thr Val Lys Leu Asp Thr Met Ile Phe	140		145		150
Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro Gly Ser Phe	155		160		165

Lys

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATG ATT GCA GTC TTC ACC CTC ACT GGA GCT GTG GTG CTG CTC CTG	45
Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu	15
1 5 10	
CTC GTC GCT CTC CTG ATG CTC AGA AAA TAT AGA AAA GAT TAT GAA	90
Leu Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu	30
20 25	
CTT CGT CAG AAA AAA TGG TCC CAC ATT CCT CCT GAA AAT ATC TTT	135
Leu Arg Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe	45
35 40	
CCT CTG GAG ACC AAT GAG ACC AAT CAT GTT AGC CTC AAG ATC GAT	180
Pro Leu Glu Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp	60
50 55	
GAT GAC AAA AGA CGA GAT ACA ATC CAG AGA CTA CGA CAG TGC AAA	225
Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys	75
65 70	
TAC GAC AAA AAG CGA GTG ATT CTC AAA GAT CTC AAG CAC AAT GAT	270
Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu Lys His Asn Asp	90
80 85	
GGT AAT TTC ACT GAA AAA CAG AAG ATA GAA TTG AAC AAG TTG CTT	315
Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu	105
95 100	
CAG AAA GAC TAT TAC AAC CTG ACC AAG TTC TAC GGC ACA GTG AAA	360
Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys	120
110 115	
CTT GAT ACC ATG ATC TTC GGG GTG ATA GAA TAC TGT GAG AGA GGA	405
Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly	135
125 130	

TCC CCT CCG GGA AGT TTT AAA
 Ser Pro Pro Gly Ser Phe Lys
 140

426

- (2) INFORMATION FOR SEQ ID NO:53:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 142 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Met Ile Ala Val Phe Thr Leu Thr Gly Ala Val Val Leu Leu Leu
 1 5 10 15
 Leu Val Ala Leu Leu Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu
 20 25 30
 Leu Arg Gln Lys Lys Trp Ser His Ile Pro Pro Glu Asn Ile Phe
 35 40 45
 Pro Leu Glu Thr Asn Glu Thr Asn His Val Ser Leu Lys Ile Asp
 50 55 60
 Asp Asp Lys Arg Arg Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys
 65 70 75
 Tyr Asp Lys Lys Arg Val Ile Leu Lys Asp Leu Lys His Asn Asp
 80 85 90
 Gly Asn Phe Thr Glu Lys Gln Lys Ile Glu Leu Asn Lys Leu Leu
 95 100 105
 Gln Lys Asp Tyr Tyr Asn Leu Thr Lys Phe Tyr Gly Thr Val Lys
 110 115 120
 Leu Asp Thr Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly
 125 130 135
 Ser Pro Pro Gly Ser Phe Lys
 140

- (2) INFORMATION FOR SEQ ID NO:54:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATG CTC AGA AAA TAT AGA AAA GAT TAT GAA CTT CGT CAG AAA AAA 45
 Met Leu Arg Lys Tyr Arg Lys Asp Tyr Glu Leu Arg Gln Lys Lys
 1 5 10 15
 TGG TCC CAC ATT CCT CCT GAA AAT ATC TTT CCT CTG GAG ACC AAT 90
 Trp Ser His Ile Pro Pro Glu Asn Ile Phe Pro Leu Glu Thr Asn
 20 25 30
 GAG ACC AAT CAT GTT AGC CTC AAG ATC GAT GAT GAC AAA AGA CGA 135
 Glu Thr Asn His Val Ser Leu Lys Ile Asp Asp Asp Lys Arg Arg
 35 40 45
 GAT ACA ATC CAG AGA CTA CGA CAG TGC AAA TAC GAC AAA AAG CGA 180
 Asp Thr Ile Gln Arg Leu Arg Gln Cys Lys Tyr Asp Lys Lys Arg
 50 55 60
 GTG ATT CTC AAA GAT CTC AAG CAC AAT GAT GGT AAT TTC ACT GAA 225

[illegible]

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Met	Leu	Arg	Lys	Tyr	Arg	Lys	Asp	Tyr	Glu	Leu	Arg	Gln	Lys	Lys	1	5	10	15
Trp	Ser	His	Ile	Pro	Pro	Glu	Asn	Ile	Phe	Pro	Leu	Glu	Thr	Asn	20	25	30	
Glu	Thr	Asn	His	Val	Ser	Leu	Lys	Ile	Asp	Asp	Asp	Lys	Arg	Arg	35	40	45	
Asp	Thr	Ile	Gln	Arg	Leu	Arg	Gln	Cys	Lys	Tyr	Asp	Lys	Lys	Arg	50	55	60	
Val	Ile	Leu	Lys	Asp	Leu	Lys	His	Asn	Asp	Gly	Asn	Phe	Thr	Glu	65	70	75	
Lys	Gln	Lys	Ile	Glu	Leu	Asn	Lys	Leu	Leu	Gln	Lys	Asp	Tyr	Tyr	80	85	90	
Asn	Leu	Thr	Lys	Phe	Tyr	Gly	Thr	Val	Lys	Leu	Asp	Thr	Met	Ile	95	100	105	
Phe	Gly	Val	Ile	Glu	Tyr	Cys	Glu	Arg	Gly	Ser	Pro	Pro	Gly	Ser	110	115	120	
Phe	Lys																	

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 57 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

ATG	ATC	TTC	GGG	GTG	ATA	GAA	TAC	TGT	GAG	AGA	GGA	TCC	CCT	CCG	45
Met	Ile	Phe	Gly	Val	Ile	Glu	Tyr	Cys	Glu	Arg	Gly	Ser	Pro	Pro	
1				5					10					15	
GGA AGT TTT AAA															57

Gly Ser Phe Lys

- (2) INFORMATION FOR SEQ ID NO:57:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 19 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Met Ile Phe Gly Val Ile Glu Tyr Cys Glu Arg Gly Ser Pro Pro
 1 5 10 15

Gly Ser Phe Lys

- (2) INFORMATION FOR SEQ ID NO:58:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ATG ATA TTA CAG GCC GGG GCC CTC AGA TCC
 Met Ile Leu Gln Ala Gly Ala Leu Arg Ser
 1 5 10

30

- (2) INFORMATION FOR SEQ ID NO:59:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met Ile Leu Gln Ala Gly Ala Leu Arg Ser
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:60:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

~~ATG AAC TTC GTC AGA AAA AAT GGT CCC ACA TTC CTC CTG AAA ATA~~
 Met Asn Phe Val Arg Lys Asn Gly Pro Thr Phe Leu Leu Lys Ile
 1 5 10 15

45

TCT TTC CTC TGG AGA CCA ATG AGA CCA ATC ATG TTA GCC TCA AGA
 Ser Phe Leu Trp Arg Pro Met Arg Pro Ile Met Leu Ala Ser Arg
 20 25 30

90

TCG ATG ATG ACA AAA GAC GAG ATA CAA TCC AGA GAC TAC GAC AGT
 Ser Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser
 35 40 45

135

GCA AAT ACG ACA AAA AGC GAG
 Ala Asn Thr Thr Lys Ser Glu
 50

156

- (2) INFORMATION FOR SEQ ID NO:61:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 52 amino acids

- (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
Met Asn Phe Val Arg Lys Asn Gly Pro Thr Phe Leu Leu Lys Ile
 1              5              10              15
Ser Phe Leu Trp Arg Pro Met Arg Pro Ile Met Leu Ala Ser Arg
              20              25              30
Ser Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser
              35              40              45
Ala Asn Thr Thr Lys Ser Glu
              50
```

- (2) INFORMATION FOR SEQ ID NO:62:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
ATG AGA CCA ATC ATG TTA GCC TCA AGA TCG ATG ATG ACA AAA GAC      45
Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp
 1              5              10              15
GAG ATA CAA TCC AGA GAC TAC GAC AGT GCA AAT ACG ACA AAA AGC      90
Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser
              20              25              30
GAG
Glu
                              93
```

- (2) INFORMATION FOR SEQ ID NO:63:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 31 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
Met Arg Pro Ile Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp
 1              5              10              15
Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser
              20              25              30
Glu
```

- (2) INFORMATION FOR SEQ ID NO:64:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 81 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
ATG TTA GCC TCA AGA TCG ATG ATG ACA AAA GAC GAG ATA CAA TCC      45
Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu Ile Gln Ser
 1              5              10              15
AGA GAC TAC GAC AGT GCA AAT ACG ACA AAA AGC GAG
                              81
```

Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu
20 25

- (2) INFORMATION FOR SEQ ID NO:65:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Met Leu Ala Ser Arg Ser Met Met Thr Lys Asp Glu Ile Gln Ser
1 5 10 15

Arg Asp Tyr Asp Ser Ala Asn Thr Thr Lys Ser Glu
20 25

- (2) INFORMATION FOR SEQ ID NO:66:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 63 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ATG ATG ACA AAA GAC GAG ATA CAA TCC AGA GAC TAC GAC AGT GCA 45
 Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala
1 5 10 15

AAT ACG ACA AAA AGC GAG 63
 Asn Thr Thr Lys Ser Glu
20

- (2) INFORMATION FOR SEQ ID NO:67:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Met Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala
1 5 10 15

Asn Thr Thr Lys Ser Glu
20

- (2) INFORMATION FOR SEQ ID NO:68:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ATG ACA AAA GAC GAG ATA CAA TCC AGA GAC TAC GAC AGT GCA AAT 45
 Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn
1 5 10 15

ACG ACA AAA AGC GAG 60
 Thr Thr Lys Ser Glu
20

- (2) INFORMATION FOR SEQ ID NO:69:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids
 (B) TYPE: amino acid

- (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Met Thr Lys Asp Glu Ile Gln Ser Arg Asp Tyr Asp Ser Ala Asn
1 5 10 15

Thr Thr Lys Ser Glu
20

- (2) INFORMATION FOR SEQ ID NO:70:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATG GTC CCA CAT TCC TCC 18
Met Val Pro His Ser Ser
1 5

- (2) INFORMATION FOR SEQ ID NO:71:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Met Val Pro His Ser Ser
1 5

- (2) INFORMATION FOR SEQ ID NO:72:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

ATG ATG GTA ATT TCA CTG AAA AAC AGA AGA 30
Met Met Val Ile Ser Leu Lys Asn Arg Arg
1 5 10

- (2) INFORMATION FOR SEQ ID NO:73:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: protein
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Met Met Val Ile Ser Leu Lys Asn Arg Arg
1 5 10

- (2) INFORMATION FOR SEQ ID NO:74:
(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

ATG GTA ATT TCA CTG AAA AAC AGA AGA 27
Met Val Ile Ser Leu Lys Asn Arg Arg
1 5

- (2) INFORMATION FOR SEQ ID NO:75:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Met Val Ile Ser Leu Lys Asn Arg Arg
 1 5

- (2) INFORMATION FOR SEQ ID NO:76:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

ATG GCG GCC GGG AGC ATG CGA CGT CGG CCC ATT CGC CCT ATA
Met Ala Ala Gly Ser Met Arg Arg Arg Pro Ile Arg Pro Ile
 1 5 10

42

- (2) INFORMATION FOR SEQ ID NO:77:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Met Ala Ala Gly Ser Met Arg Arg Arg Pro Ile Arg Pro Ile
 1 5 10

- (2) INFORMATION FOR SEQ ID NO:78:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ATG CGA CGT CGG CCC ATT CGC CCT ATA
Met Arg Arg Arg Pro Ile Arg Pro Ile
 1 5

27

- (2) INFORMATION FOR SEQ ID NO:79:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met Arg Arg Arg Pro Ile Arg Pro Ile
 1 5

- (2) INFORMATION FOR SEQ ID NO:80:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ATG ACA CAA TTT CCT
Met Thr Gln Phe Pro

15

1 5

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Met Thr Gln Phe Pro

1 5

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH:
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

TGGAGTGGGCTGAGGGACTCCACTAGAGGCTGTCCATCTGGATTCCCTGCCTCCCTAGGAGCCCAACAGAGCAAAGCAAG 80
TGGGCACAAGGAGTATGGTTCTAACGTGATTGGGGTATGAAGACGTGCTGTTGGACTTGGCTTTGTGOTCACTGCTCT
TCCAGCCCGGGTGGCTGTCTTTAGTTCCCA/GG
TGTGCTTCCCTTAAATTTTACTGTGAACCCCTACTTTTATGTATTCCGATGCTCTGATTTCTATACTTACCTTACCTT
GCCGGAGTAGCACCCTGTGAAGGCCCTCGACCTACTCAGGAAAAATTTCAAATGCACAACCGGATGGCTGTGTCTCTCATAGGG
CCCTCATGTACATACTCCACCTTCCAGATGTACCTTGACACAGAAATGAGCTACCCCATGATTTACAGCTGGAAAGTTTGTG
ATTGTCTATGTGACTATAAAGAAACCTTAACCAGGCTGATGTCTCCAGCTTGAAGAAAGTTGATGTACTTTTGGTTAACTTTT
GGAAAACCAACGATCTGCCCTTCAAACCTTATTTCTGGAGCAGCTTGTATGTTTACAAGAAATGCTACAGAACTTGAGGAC
TGTCTTCTGGTACCTTAAATGCTCTGGAGGCTAGCGTTTCTTATTTCTCCACGAACTTGGCTTTAAGGTTGTTAAGACA
AGATAAGGAGTTTCAAGGATATCTTAATGGACCAACAGGAAAGCAATGTGATTTATTTATGTGTGGTGGTCCAGAGTTCC
TCTACAAGCTGAAGGGTGACCGAGCAGTGGCTGAAGACATTGTCAATTATCTAGTGGATCTTTTCAAAGACAGTACTTG
GAGGACAATGTACAGCCCTTACTATATGAAAAATGTCTTGTCTGACCGCTGTTCTCTGGGAATTTCCCTTCTAAATAG
CTCTTTCTCCAGGAATCTATACCAACAAAAAGAGACTTTCTGTCTTGGCTATTTGAATGGAAATCTCTCTTTGGACATA
TGCTGAAGATATTTCTTGAAGAAATGGAGAAAAATATTACCACCCCAAAATTTGCTCAATGCTTCAGGAATCTCACTTTTGAA
GGGATGACCGTCCAGTACCCTTGGATGACTGGGGGGATGTTGACAGTACCATGCTGCTTCTGTATACCTCTGTGGACAC
CAAGAAATACAAAGTTTCTTTTGACCTATGATACCCACGTAAATAAGACCCTATCTGTGGATATGAGCCCACTTCACTT
GGAAGAACTCTAAACTTCTTAATGATATTACAGGCCCGGGCCCTCAGATCTTGAATGATTGCAGTCTTCAACCTCACTGGA
GCTGTGGTGTCTCTCTGTCTGTCTCTCTGTATGCTCAGAAAAATATAGAAAAAGATTATGAATCTCTCAGAAAAAATG
GTCCACATTTCTCTTGAAGAAATATCTTTCTCTGGAGACCAATGAGACCAATCATGTTAGCTTCAAGATCGATGATGACA
AAGACGAGATACAACTCAGAGACTACGACAGTGAATAACGTCAAAAAGCGAGTGTATCTCAAAGATCTCAAGCACAAAT
GATGGTAATTTCACTGAAAAACAGAAAGATAGAATTGAACAAGTTGCTTCAAGTTGACTATTACACCTTAACCAAGTTCTA
CGGACAGTCAAACTGGATACCATGATCTTCTGGGGTGATAGAATACTGTGAGAGAGGAATCTCTCCGGGAATTTTAAATG
ACACAATTTCTTACCCTGATGGCACATTTATGGATTGGGAGTTTAAGATCTCTGTCTTTGTATGACATTGCTAAGGGAAATG
TCATATCTGCACTCCAGTAAGACAGAAAGTCCATGGTGTCTGAAATCTACCAACTGCGTAGTGGACAGTGAATGGTGGT
GAAGATCACTGATTTTGGCTGCAATTTCCATTTTGCTTCAAAAAAGGACCTGTGGACAGCTCCAGAGCACCTCCGCCAAG
CCAACATCTCTCAGAAAGGAGATGTGTACAGCTATGGGATCATCGCACAGGAGATCATTTCTGCGGAAAGAAACCTCTTAC
ACTTTGAGCTGTCTGGGACCGGAATCAGAAGATTTTCAAGATGGAATAATTCCAATGGAATGAACCTTCCGCCCAATTT
ATTTCTGGAACAGCAGAGGAAAAAGAGCTAGAAAGTTGACTACTTGTAAAAAATGTTGGGAGGAAGATCCAGAAAAAG
GACCAAGATTTCAAAAAAATGAGACTACACTTGCCTAAGATAATTTGACTTTTTCATGACCAAAAAAATGAAAGCTATATG
GATACCTTGATCCGACGTCTACAGCTATATTTCTGAAACCTGGAACATCTGGTAGAGGAAAGGACACAGCTGTACAAAGGC
AGAGAGGGACAGGGCTGACAGACTTAACCTTATGTTGCTTCAAGGCTAGTGGTAAAGTCTCTGAAGGAGAAAGGCTTTG
TGGAGCCGGAATATATGAGGAAGTTACAACTACTTCAGTGACATTGTAGGTTTCACTACTATCTGCAAAATACAGCACC
CCCATGGAAGTGGTGGACATGCTTAATGACATCTATAAGAGTTTGGACACATTTGTGATCATCATGATCTCTACAAGGT
GGAAACCATCTGGTGTATGCTATCATGGTGGCTAGTGGTTTGGCTAAGAGAAATGGCAATCGGCAATGCAATAGACATTGCCA
AGATGGCCCTTGGAAATCTCAGCTTCAATGGGGACCTTTGAGCTGGAGCATCTTCTTGGCTTCCCAATATGGATTGCGAAT
GGAGTTCACTCTGGTCTCTGTGCTGTCTGAGTTTGTGGGAATCAAGATGCTTCTGTTATTTGTCTATTTGGAGATACGGTCAA
CACAGCTCTAGGATGGAATCCACTGGCTTCCCTTTGAGAAATCACGTGAGTGGCTTCCACCATAGCCATCCTGAAGAGAA
CTGAGTGCCAGTTCTTTATGAAGTGAGAGGAGAAACATACTTAAAGGGAAAGAGGAAATGAGACTACCTTACTGGCTGACT
GGGATGAAGGACCAGAAATTCACCTGCCAACCCCTCTTACTTGTGGAGATCAACAGCTTTTGCAGGCAAGAAATTTTCAGA
CATGATTGCCAATCTTTACAGAAAGACAGGACAGGAGGATTAAGAGCCAAACCCAGACGGGTAGCCAGCTATAAAA
AAGGCACTTGGAAATCTTGCAGCTGAATACACAGACAAGGAGAGCACCCTATTTTAAACCTAAATGAGGTATAAGGAC
TCACACAAATTAATAACAGCTGCAGTGAAGGCCAGGACCCCTCAGGTGTCTTGAAGCTTACTTTTCTGAGACCTCATGA
GGCAGAAATGTCTTAGGCTTGGCTGCCCCTGTTTGGACCATGGACTTTCTTTGCTATGAATCAGATGTGTCTCTCAGTGAAT
AACTACCTTCCACTCTGGAACCTTATTTCCAGCAGTTGTTCCAGGGAGCTTCTACCTGGAAGAAAGAAATTTCAATTTA
TTTGTGTTGTTTATTTTATCGTTTGTGTTTACTGGCTTTCTCTGTATTCTAAGATTTTAAATGTCTAATTTA
TATTTTAAATACCCATCTTCAATTAAGTATAATTAACCTATAATTTTGCAGAAAAATGCTATATATAGGCAAGAATA
AAAGCTAAAGGTTTCCCAAAAAA